

SEQUENCE LISTING

<110> Albani, Salvatore

<120> METHODS FOR ISOLATION, QUANTIFICATION,
CHARACTERIZATION AND MODULATION OF
ANTIGEN-SPECIFIC T CELLS

<130> 031544.0004.CIP

<140> NOT YET ASSIGNED

<141> 2001-01-09

<150> 60/105,018

<151> 1998-10-20

<150> 09/421,506

<151> 1999-10-19

<150> PCT/US99/2466

<151> 1999-10-19

<160> 24

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from third hyper V
region of IE molecule Mus musculus

<400> 1

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Ala

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized peptide derived from boe I protein
of Epstein Barr virus

<400> 2

Thr	Arg	Asp	Asp	Ala	Glu	Tyr	Leu	Leu	Gly	Arg	Glu	Ser	Val	Leu
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09756937-010901

<210> 3
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the hemophilus
 influenza virus

<400> 3
 Thr Ser Phe Pro Met Arg Gly Asp Leu Ala Lys Arg Glu Pro Asp Lys
 1 5 10 15

<210> 4
 <211> 36
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the TCR receptor
 gene of Mus musculus

<400> 4
 Leu His Ile Ser Ala Val Asp Pro Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser
 1 5 10 15
 Ser Gln Glu Phe Phe Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly Thr
 20 25 30
 Arg Leu
 35

<210> 5
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the influenza virus

<400> 5
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the influenza virus

<400> 6
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
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097553-04004

<210> 7
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide totally artificial

<220>
 <223> Xaa in position 2 stands for cyclohexylalanine

<400> 7
 Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala
 1 5 10

<210> 8
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the influenza virus

<400> 8
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

<210> 9
 <211> 17
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 <213> Artificial Sequence

<220>
 <223> Synthesized peptide derived from the ovalbumin
 of Mus musculus

<400> 9
 Ile Ser Gln Ala Val His Ala Ala His Ala Glu Ile Asn Glu Ala Gly
 1 5 10 15
 Arg

<210> 10
 <211> 15
 <212> PRT
 <213> E. coli

<220>
 <223> dnaJp1 heat shock protein

<400> 10
 Gln Lys Arg Ala Ala Tyr Asp Gln Tyr Gly His Ala Ala Phe Glu
 1 5 10 15

0975533-01001

<210> 11
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 11
 Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr Gly
 1 5 10 15

<210> 12
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 12
 Gly Ile Leu Gly Phe Val Phe Thr Leu
 1 5

<210> 13
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 13
 Val Lys Leu Gly Glu Phe Tyr Asn Gln
 1 5

<210> 14
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 14
 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
 1 5 10

<210> 15
 <211> 313
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion constructs with human and bacterial sequences

<400> 15
 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 1 5 10 15
 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 20 25 30
 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu

0975993-00904

35	40	45
Ser Cys Gly His Asn Val	Ser Val Glu Glu Leu	Ala Gln Thr Arg Ile
50	55	60
Tyr Trp Gln Lys Glu Lys	Lys Met Val Leu Thr	Met Met Ser Gly Asp
65	70	75
Met Asn Ile Trp Pro Glu	Tyr Lys Asn Arg Thr	Ile Phe Asp Ile Thr
85	90	95
Asn Asn Leu Ser Ile Val	Ile Leu Ala Leu Arg	Pro Ser Asp Glu Gly
100	105	110
Thr Tyr Glu Cys Val Val	Leu Lys Tyr Glu Lys	Asp Ala Phe Lys Arg
115	120	125
Glu His Leu Ala Glu Val	Thr Leu Ser Val Lys	Ala Asp Phe Pro Thr
130	135	140
Pro Ser Ile Ser Asp Phe	Glu Ile Pro Thr Ser	Asn Ile Arg Arg Ile
145	150	155
Ile Cys Ser Thr Ser Gly	Gly Phe Pro Glu Pro	His Leu Ser Trp Leu
165	170	175
Glu Asn Gly Glu Glu Leu	Asn Ala Ile Asn Thr	Thr Val Ser Gln Asp
180	185	190
Pro Glu Thr Glu Leu Tyr	Ala Val Ser Glu Phe	Gly Gly Ser Gly Gly
195	200	205
Ser Ala Thr Pro Gln Asn	Ile Thr Asp Leu Cys	Ala Glu Tyr His Asn
210	215	220
Thr Gln Ile His Thr Leu	Asn Asp Lys Ile Phe	Ser Tyr Thr Glu Ser
225	230	235
Leu Ala Gly Lys Arg Glu	Met Ala Ile Ile Thr	Phe Lys Asn Gly Ala
245	250	255
Thr Phe Gln Val Glu Val	Pro Gly Ser Gln His	Ile Asp Ser Gln Lys
260	265	270
Lys Ala Ile Glu Arg Met	Lys Asp Thr Leu Arg	Ile Ala Tyr Leu Thr
275	280	285
Glu Ala Lys Val Glu Lys	Leu Cys Val Trp Asn	Asn Lys Thr Pro His
290	295	300
Ala Ile Ala Ala Ile Ser	Met Ala Asn	
305	310	

<210> 16

<211> 942

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 16

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gaagtgaag aagtggcaac gctgtcctgt ggtcacaatg tttctgttga agagctggca 180
caaactcgca tctactggca aaaggagaag aaaatggtgc tgactatgat gtctggggac 240
atgaatatat ggcccgagta caagaaccgg accatctttg atatacctaa taacctctcc 300
attgtgatcc tggtctgctg cccatctgac gagggcacat acgagtgtgt tgttctgaag 360
tatgaaaaag acgctttcaa gcgggaacac ctggctgaag tgacgttatc agtcaaagct 420
gacttcctta cacctagtat atctgacttt gaaattccaa cttctaatat tagaaggata 480
atttgctcaa cctctggagg ttttccagag cctcacctct cctgggttga aaatggagaa 540
gaattaaatg ccatcaacac aacagtttcc caagatcctg aaactgagct ctatgctgtt 600

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TOP SECRET

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ctagctggaa aaagagagat ggctatcatt acttttaaga atgggtgcaac ttttcaagta 780
gaagtaccag gtagtcaaca tatagattca caaaaaaaaag cgattgaaag gatgaaggat 840
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<210> 17

<211> 1056

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 17

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aaccaaagcc tgagtgaagt agtagtattt tggcaggacc aggaaaactt gggttctgaat 180
gaggtatact taggcaaaga gaaatttgac agtggttcatt ccaagtatat gggccgcaca 240
agttttgatt cggacagttg gacctgaga cttcacaatc ttcagatcaa ggacaagggc 300
ttgtatcaat gtatcatcca tcacaaaaag cccacaggaa tgattcgcac ccaccagatg 360
aattctgaac tgtcagtgct tgctaacttc agtcaacctg aaatagtacc aatttctaata 420
ataacagaaa atgtgtacat aaatttgacc tgctcatcta tacacggtta cccagaacct 480
aagaagatga gtgttttgct aagaaccaag aattcaacta tcgagtatga tgggtattatg 540
cagaaatctc aagataatgt cacagaactg tacgacgttt ccatcagctt gtctgtttca 600
ttccctgatg ttacgagcaa tatgaccatc ttctgtattc tggaaactga caagacgcgg 660
cttttatctt cacctttctc tatagagctt gaggaccctc agcctcccc agaccacgaa 720
ttcggcggct ccggtggtag cgccacacct caaaatatta ctgatttgtg tgcagaatac 780
cacaacacac aaatacatat gctaaatgat aagatatatt cgtatacaga atctctagct 840
ggaaaaagag agatggctat cattaatttt aagaatgggtg caacttttca agtagaagta 900
ccaggtagtc aacatataga ttcacaaaaa aaagcgattg aaaggatgaa ggataccctg 960
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cctcatgcga ttgcgcgaat tagtatggca aattaa 1056

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<210> 18

<211> 351

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 18

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Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu
20           25           30
Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser Glu Leu Val
35           40           45
Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu Val Tyr Leu
50           55           60
Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met Gly Arg Thr
65           70           75           80
Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn Leu Gln Ile
85           90           95

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T05070.E0605460

Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys Lys Pro Thr
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 Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser Val Leu Ala
 115 120 125
 Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile Thr Glu Asn
 130 135 140
 Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr Pro Glu Pro
 145 150 155 160
 Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr Ile Glu Tyr
 165 170 175
 Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu Leu Tyr Asp
 180 185 190
 Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr Ser Asn Met
 195 200 205
 Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu Leu Ser Ser
 210 215 220
 Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro Asp His Glu
 225 230 235 240
 Phe Gly Gly Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu
 245 250 255
 Cys Ala Glu Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile
 260 265 270
 Phe Ser Tyr Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile
 275 280 285
 Thr Phe Lys Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln
 290 295 300
 His Ile Asp Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu
 305 310 315 320
 Arg Ile Ala Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp
 325 330 335
 Asn Asn Lys Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
 340 345 350

<210> 19
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptides

<400> 19
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 Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln
 20 25 30

T05719.E009260

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<400> 22
Met Ala Ile Ser Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val
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Leu Met Ser Ala Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile
          20          25          30

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Ile Gln Ala Glu Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met
 35 40 45
 Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys
 50 55 60
 Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu
 65 70 75 80
 Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu
 85 90 95
 Ile Met Thr Lys Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro
 100 105 110
 Glu Val Thr Val Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn
 115 120 125
 Val Leu Ile Cys Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val
 130 135 140
 Thr Trp Leu Arg Asn Gly Lys Pro Val Thr Thr Gly Val Ser Glu Thr
 145 150 155 160
 Val Phe Leu Pro Arg Glu Asp His Leu Phe Arg Lys Phe His Tyr Leu
 165 170 175
 Pro Phe Leu Pro Ser Thr Glu Asp Val Tyr Asp Cys Arg Val Glu His
 180 185 190
 Trp Gly Leu Asp Glu Pro Leu Leu Lys His Trp Glu Phe Asp Ala Pro
 195 200 205
 Ser Pro Leu Pro Glu Thr Thr Glu Glu Phe Gly Gly Ser Gly Gly Ser
 210 215 220
 Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln
 225 230 235 240
 Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Gly Gly
 245 250 255
 Ser Gly Gly Ser Ala Thr Pro Gln Asn Ile Thr Asp Leu Cys Ala Glu
 260 265 270
 Tyr His Asn Thr Gln Ile His Thr Leu Asn Asp Lys Ile Phe Ser Tyr
 275 280 285
 Thr Glu Ser Leu Ala Gly Lys Arg Glu Met Ala Ile Ile Thr Phe Lys
 290 295 300
 Asn Gly Ala Thr Phe Gln Val Glu Val Pro Gly Ser Gln His Ile Asp
 305 310 315 320
 Ser Gln Lys Lys Ala Ile Glu Arg Met Lys Asp Thr Leu Arg Ile Ala
 325 330 335
 Tyr Leu Thr Glu Ala Lys Val Glu Lys Leu Cys Val Trp Asn Asn Lys
 340 345 350
 Thr Pro His Ala Ile Ala Ala Ile Ser Met Ala Asn
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<210> 23

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 23

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 aaacatgagt gtcatttctt caacgggacg gagcgggtgc ggttcttgga cagatacttc 180
 tatcaccaag aggagtacgt gcgcttcgac agcgacgtgg gggagtaccg ggcgggtgacg 240

005603-010901

gagctggggc ggctgatgc cgagtactgg aacagccaga aggacctcct ggagcagaag 300
 cgggcccggg tggacaccta ctgcagacac aactacgggg ttggtgagag cttcacagtg 360
 cagcggcgag tctatcctga ggtgactgtg tatcctgcaa agaccagacc cctgcagcac 420
 cacaacctcc tggctctgctc tgtgaatggg ttctatccag gcagcattga agtcaggtgg 480
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<210> 24

<211> 285

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion constructs with human and bacterial sequences

<400> 24

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 35 40 45
 Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr His Gln Glu
 50 55 60
 Glu Tyr Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr
 65 70 75 80
 Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln Lys Asp Leu
 85 90 95
 Leu Glu Gln Lys Arg Ala Ala Val Asp Thr Tyr Cys Arg His Asn Tyr
 100 105 110
 Gly Val Gly Glu Ser Phe Thr Val Gln Arg Arg Val Tyr Pro Glu Val
 115 120 125
 Thr Val Tyr Pro Ala Lys Thr Gln Pro Leu Gln His His Asn Leu Leu
 130 135 140
 Val Cys Ser Val Asn Gly Phe Tyr Pro Gly Ser Ile Glu Val Arg Trp
 145 150 155 160
 Phe Arg Asn Gly Gln Glu Glu Lys Thr Gly Val Val Ser Thr Gly Leu
 165 170 175
 Ile Gln Asn Gly Asp Trp Thr Phe Gln Thr Leu Val Met Leu Glu Thr
 180 185 190
 Val Pro Arg Ser Gly Glu Val Tyr Thr Cys Gln Val Glu His Pro Ser
 195 200 205
 Leu Thr Ser Pro Leu Thr Val Glu Trp Arg Ala Arg Ser Glu Ser Ala
 210 215 220
 Gln Ser Lys Gly Gly Ser Gly Gly Ser Ala Gln Leu Lys Lys Lys Leu
 225 230 235 240
 Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Gln Lys Leu Gln Ala
 245 250 255
 Leu Lys Lys Lys Leu Ala Gln Gly Ser Gly Gly Ser Ala Gly Gly Gly
 260 265 270
 Leu Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His
 275 280 285

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